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Amendments to the Claims:

A complete listing of Claims including currently amended Claim 24:

Claims 1 - 23 (Cancelled)

24. (Currently amended) A method of analyzing a subset of nucleic acids within a nucleic acid population, comprising:

(a) providing a driver population of nucleic acids and a tester population of nucleic acids;

(b) denaturing said driver population of nucleic acids and said tester population of nucleic acids;

(c) annealing said driver population to said tester population to produce a single-stranded subset of nucleic acids and a double-stranded subset of nucleic acids;

(d) immobilizing said driver population of nucleic acids to produce an unimmobilized single-stranded tester subset of nucleic acids, an immobilized double-stranded tester-driver subset of nucleic acids and an immobilized single-stranded driver subset of nucleic acids;

(e) separating said unimmobilized single-stranded tester subset of nucleic acids from said immobilized double-stranded tester-driver subset of nucleic acids and said immobilized single-stranded driver subset of nucleic acids;

(f) dissociating said immobilized double-stranded tester-driver subset of nucleic acids to produce a subset of complementary tester nucleic acids and a subset of immobilized complementary driver nucleic acids;

(g) separating said subset of complementary tester nucleic acids from said subset of immobilized complementary driver nucleic acids;

(h) hybridizing said subset of complementary tester nucleic acids to probes on a nucleic acid probe array; and

(i) determining which of said probes on said array hybridize to said subset of complementary tester nucleic acids, thereby analyzing said subset of complementary tester nucleic acids.

25. (Original) The method of claim 24, wherein said driver population is a population of genomic DNA fragments, and said tester population is mRNA or nucleic acids derived therefrom.

26. (Original) The method of claim 24, wherein said driver population is a population of genomic DNA fragments from a first source, and said tester population is genomic DNA from a second source.

27. (Original) The method of claim 26, wherein said tester population is from a genome of a first individual, and said driver population is from a genome of a different individual of a same species as said first individual.

28. (Original) The method of claim 26, wherein said tester population is from a genome of a first individual, and said driver population is from a genome of an individual of a different species than said first individual.

29. (Original) The method of claim 24, wherein either said driver population or said tester population or both said driver and said tester populations is a PCR amplification product.

30. (Original) The method of claim 24, wherein said driver population is from a plurality of noncontiguous regions of a genome of a species.

31. (Original) The method of claim 30, wherein said driver population is from at least ten noncontiguous regions.

32. (Original) The method of claim 24, wherein said driver population is mRNA or nucleic acids derived therefrom, and said tester population is genomic DNA.

33. (Original) The method of claim 24, wherein said driver population is mRNA or nucleic acids derived therefrom from a first source, and said tester population is mRNA or nucleic acids derived therefrom from a second source.

34. (Original) The method of claim 33, wherein said first source is from a tissue of a first species, and said second source is from a same tissue of a different species.

35. (Original) The method of claim 33, wherein said first source is from a first tissue of a first species, and said second source is from a different tissue of said first species.

36. (Original) The method of claim 24, wherein said immobilizing step is performed before said annealing step.

37. (Original) The method of claim 24, wherein said immobilizing step is performed before said first denaturing step.

38. (Original) The method of claim 24, wherein said driver population of nucleic acids each bear a tag by which said driver population can be immobilized to a binding moiety with affinity for said tag.

39. (Original) The method of claim 38, wherein said tag is biotin, and said binding moiety is avidin or streptavidin.

40. (Original) The method of claim 39, wherein said first separating step is performed by immobilizing said driver population of nucleic acids and tester population of nucleic acids hybridized to said driver population via said tags on said driver population.